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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/873,106B

DATE: 05/02/2002

TIME: 17:04:59

Input Set : A:\10621021004 sub seq.txt

Output Set: N:\CRF3\05022002\I873106B.raw

ENTERED

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4 <110> APPLICANT: Reinherz, Ellis L.
5      Freund, Christian
6      Li, Jing
7      Nishizawa, Kazuhisa
8      Wagner, Gerhard
10 <120> TITLE OF INVENTION: Cloning and Characterization of a CD2
11      Binding Protein (CD2BP2)
14 <130> FILE REFERENCE: 1062.1021-004
16 <140> CURRENT APPLICATION NUMBER: US 09/873,106B
17 <141> CURRENT FILING DATE: 2001-06-01
19 <150> PRIOR APPLICATION NUMBER: US 60/111,007
20 <151> PRIOR FILING DATE: 1998-12-04
22 <150> PRIOR APPLICATION NUMBER: US 60/115,647
23 <151> PRIOR FILING DATE: 1999-01-13
25 <150> PRIOR APPLICATION NUMBER: PCT/US99/26993
26 <151> PRIOR FILING DATE: 1999-11-15
28 <160> NUMBER OF SEQ ID NOS: 25
30 <170> SOFTWARE: FastSEQ for Windows Version 4.0
32 <210> SEQ ID NO: 1
33 <211> LENGTH: 1299
34 <212> TYPE: DNA
35 <213> ORGANISM: Homo sapiens
37 <220> FEATURE:
38 <221> NAME/KEY: CDS
39 <222> LOCATION: (121)...(1143)
41 <400> SEQUENCE: 1
42 agtcctcttc cgggtgatgg cggcgggtgc cccggatgta gccctggcgc aagcatctct 60
43 tcttttttcc acctgcctt ccgcggatgc ccagcttgag aaacacctct ttgccccgtc 120
44 atg cca aag agg aaa gtg acc ttc caa ggc gtg gga gat gag gat 168
45 Met Pro Lys Arg Lys Val Thr Phe Gln Gly Val Gly Asp Glu Glu Asp
46 1 5 10 15
48 gag gat gaa atc att gtc ccc aag aag aag ctg gtg gac cct gtg gct 216
49 Glu Asp Glu Ile Ile Val Pro Lys Lys Lys Leu Val Asp Pro Val Ala
50 20 25 30
52 ggg tca ggg ggt cct ggg agc cgc ttt aaa ggc aaa cac tct ttg gat 264
53 Gly Ser Gly Gly Pro Gly Ser Arg Phe Lys Gly Lys His Ser Leu Asp
54 35 40 45
56 agc gat gag gag gag gat gat gat gat ggg ggg tcc agc aaa tat gac 312
57 Ser Asp Glu Glu Glu Asp Asp Asp Asp Gly Gly Ser Ser Lys Tyr Asp
58 50 55 60
60 atc ttg gcc tca gag gat gta gaa ggt cag gag gca gcc aca ctc ccc 360
61 Ile Leu Ala Ser Glu Asp Val Glu Gly Gln Glu Ala Ala Thr Leu Pro
62 65 70 75 80

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64 agc gag ggg ggt ggt cgg atc aca ccc ttt aac ctg cag gag gag atg 408
65 Ser Glu Gly Gly Gly Arg Ile Thr Pro Phe Asn Leu Gln Glu Glu Met
66      85      90      95
68 gag gaa ggc cac ttt gat gcc gat ggc aac tac ttc ctg aac cgg gat 456
69 Glu Glu Gly His Phe Asp Ala Asp Gly Asn Tyr Phe Leu Asn Arg Asp
70      100      105      110
72 gct cag atc cga gac agc tgg ctg gac aac att gac tgg gtg aag atc 504
73 Ala Gln Ile Arg Asp Ser Trp Leu Asp Asn Ile Asp Trp Val Lys Ile
74      115      120      125
76 cgg gag cgg cca cct ggc cag cgc cag gcc tca gac tcg gag gag gag 552
77 Arg Glu Arg Pro Pro Gly Gln Arg Gln Ala Ser Asp Ser Glu Glu Glu
78      130      135      140
80 gac agc ttg ggc cag acc tca atg agt gcc caa gcc ctc ttg gag gga 600
81 Asp Ser Leu Gly Gln Thr Ser Met Ser Ala Gln Ala Leu Leu Glu Gly
82 145      150      155      160
84 ctt ttg gag ctc cta ttg cct aga gag aca gtg gct ggg gca ctg agg 648
85 Leu Leu Glu Leu Leu Leu Pro Arg Glu Thr Val Ala Gly Ala Leu Arg
86      165      170      175
88 cgt ctg ggg gcc cga gga gga ggc aaa ggg aga aag ggg cct ggg caa 696
89 Arg Leu Gly Ala Arg Gly Gly Gly Lys Gly Arg Lys Gly Pro Gly Gln
90      180      185      190
92 ccc agt tcc cct cag cgc ctg gac cgg ctc tcc ggg ttg gcc gac cag 744
93 Pro Ser Ser Pro Gln Arg Leu Asp Arg Leu Ser Gly Leu Ala Asp Gln
94      195      200      205
96 atg gtg gcc cgg ggc aac ctt ggt gtg tac cag gaa aca agg gaa cgg 792
97 Met Val Ala Arg Gly Asn Leu Gly Val Tyr Gln Glu Thr Arg Glu Arg
98      210      215      220
100 ttg gct atg cgt ctg aag ggt ttg ggg tgt cag acc cta gga ccc cac 840
101 Leu Ala Met Arg Leu Lys Gly Leu Gly Cys Gln Thr Leu Gly Pro His
102 225      230      235      240
104 aat ccc aca ccc cca ccc tcc ctg gac atg ttc gct gag gag ttg gcg 888
105 Asn Pro Thr Pro Pro Pro Ser Leu Asp Met Phe Ala Glu Glu Leu Ala
106      245      250      255
108 gag gag gaa ctg gag acc cca acc cct acc cag aga gga gaa gca gag 936
109 Glu Glu Glu Leu Glu Thr Pro Thr Pro Thr Gln Arg Gly Glu Ala Glu
110      260      265      270
112 tcg cgg gga gat ggt ctg gtg gat gtg atg tgg gaa tat aag tgg gag 984
113 Ser Arg Gly Asp Gly Leu Val Asp Val Met Trp Glu Tyr Lys Trp Glu
114      275      280      285
116 aac acg ggg gat gcc gag ctg tat ggg ccc ttc acc agc gcc cag atg 1032
117 Asn Thr Gly Asp Ala Glu Leu Tyr Gly Pro Phe Thr Ser Ala Gln Met
118      290      295      300
120 cag acc tgg gtg agt gaa ggc tac ttc ccg gac ggt gtt tat tgc cgg 1080
121 Gln Thr Trp Val Ser Glu Gly Tyr Phe Pro Asp Gly Val Tyr Cys Arg
122 305      310      315      320
124 aag ctg gac ccc cct ggt ggt cag ttc tac aac tcc aaa cgc att gac 1128
125 Lys Leu Asp Pro Pro Gly Gly Gln Phe Tyr Asn Ser Lys Arg Ile Asp
126      325      330      335
128 ttt gac ctc tac acc tgagcctgct gggggccag tttggtgggc ccttctttcc 1183

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129 Phe Asp Leu Tyr Thr
130                               340
132 tggactttgt ggaggaggca ccaagtgtct caggcagcga ggaaattgga ggccattttt 1243
133 cagtcaattt ccctttccca ataaaagcct tagttgtgta aaaaaaaaaa aaaaaa 1299
135 <210> SEQ ID NO: 2
136 <211> LENGTH: 341
137 <212> TYPE: PRT
138 <213> ORGANISM: Homo sapiens
140 <400> SEQUENCE: 2
141 Met Pro Lys Arg Lys Val Thr Phe Gln Gly Val Gly Asp Glu Glu Asp
142 1 5 10 15
143 Glu Asp Glu Ile Ile Val Pro Lys Lys Lys Leu Val Asp Pro Val Ala
144 20 25 30
145 Gly Ser Gly Gly Pro Gly Ser Arg Phe Lys Gly Lys His Ser Leu Asp
146 35 40 45
147 Ser Asp Glu Glu Glu Asp Asp Asp Gly Gly Ser Ser Lys Tyr Asp
148 50 55 60
149 Ile Leu Ala Ser Glu Asp Val Glu Gly Gln Glu Ala Ala Thr Leu Pro
150 65 70 75 80
151 Ser Glu Gly Gly Gly Arg Ile Thr Pro Phe Asn Leu Gln Glu Glu Met
152 85 90 95
153 Glu Glu Gly His Phe Asp Ala Asp Gly Asn Tyr Phe Leu Asn Arg Asp
154 100 105 110
155 Ala Gln Ile Arg Asp Ser Trp Leu Asp Asn Ile Asp Trp Val Lys Ile
156 115 120 125
157 Arg Glu Arg Pro Pro Gly Gln Arg Gln Ala Ser Asp Ser Glu Glu Glu
158 130 135 140
159 Asp Ser Leu Gly Gln Thr Ser Met Ser Ala Gln Ala Leu Leu Glu Gly
160 145 150 155 160
161 Leu Leu Glu Leu Leu Leu Pro Arg Glu Thr Val Ala Gly Ala Leu Arg
162 165 170 175
163 Arg Leu Gly Ala Arg Gly Gly Gly Lys Gly Arg Lys Gly Pro Gly Gln
164 180 185 190
165 Pro Ser Ser Pro Gln Arg Leu Asp Arg Leu Ser Gly Leu Ala Asp Gln
166 195 200 205
167 Met Val Ala Arg Gly Asn Leu Gly Val Tyr Gln Glu Thr Arg Glu Arg
168 210 215 220
169 Leu Ala Met Arg Leu Lys Gly Leu Gly Cys Gln Thr Leu Gly Pro His
170 225 230 235 240
171 Asn Pro Thr Pro Pro Pro Ser Leu Asp Met Phe Ala Glu Glu Leu Ala
172 245 250 255
173 Glu Glu Glu Leu Glu Thr Pro Thr Pro Thr Gln Arg Gly Glu Ala Glu
174 260 265 270
175 Ser Arg Gly Asp Gly Leu Val Asp Val Met Trp Glu Tyr Lys Trp Glu
176 275 280 285
177 Asn Thr Gly Asp Ala Glu Leu Tyr Gly Pro Phe Thr Ser Ala Gln Met
178 290 295 300
179 Gln Thr Trp Val Ser Glu Gly Tyr Phe Pro Asp Gly Val Tyr Cys Arg
180 305 310 315 320

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181 Lys Leu Asp Pro Pro Gly Gly Gln Phe Tyr Asn Ser Lys Arg Ile Asp
182                               325                               330                               335
183 Phe Asp Leu Tyr Thr
184                               340
187 <210> SEQ ID NO: 3
188 <211> LENGTH: 26
189 <212> TYPE: PRT
190 <213> ORGANISM: Homo sapiens
192 <400> SEQUENCE: 3
193 Gly Asp Ala Glu Leu Tyr Gly Pro Phe Thr Ser Ala Gln Met Gln Thr
194 1                               5                               10                               15
195 Trp Val Ser Glu Gly Tyr Phe Pro Asp Gly
196                               20                               25
199 <210> SEQ ID NO: 4
200 <211> LENGTH: 27
201 <212> TYPE: PRT
202 <213> ORGANISM: Caenorhabditis elegans
204 <400> SEQUENCE: 4
205 Gly Pro Asp Ser Glu Lys Tyr Gly Pro Tyr Met Ser Lys Asp Met Leu
206 1                               5                               10                               15
207 Phe Trp Leu Gln Ala Gly Tyr Phe Asn Asp Gly
208                               20                               25
211 <210> SEQ ID NO: 5
212 <211> LENGTH: 27
213 <212> TYPE: PRT
214 <213> ORGANISM: Caenorhabditis elegans
216 <400> SEQUENCE: 5
217 Asp Pro Thr Glu Thr Arg Arg Gly Pro Phe Pro Lys Asp Gln Met Asn
218 1                               5                               10                               15
219 Val Trp Phe Lys Ala Gly Tyr Phe Thr Asp Glu
220                               20                               25
223 <210> SEQ ID NO: 6
224 <211> LENGTH: 27
225 <212> TYPE: PRT
226 <213> ORGANISM: Caenorhabditis elegans
228 <400> SEQUENCE: 6
229 Asp Asp Arg Gly Thr Val Gln Gly Pro Tyr Gly Ala Ser Thr Val Leu
230 1                               5                               10                               15
231 Asp Trp Tyr Gln Lys Gly Tyr Phe Ser Asp Asn
232                               20                               25
235 <210> SEQ ID NO: 7
236 <211> LENGTH: 29
237 <212> TYPE: PRT
238 <213> ORGANISM: Saccharomyces cerevisiae
240 <400> SEQUENCE: 7
241 Asp Thr Gln Gly Gln Ile His Gly Pro Phe Thr Thr Gln Met Met Ser
242 1                               5                               10                               15
243 Gln Trp Tyr Ile Gly Gly Leu Glu Tyr Phe Ala Ser Thr
244                               20                               25

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Input Set : A:\10621021004 sub seq.txt

Output Set: N:\CRF3\05022002\I873106B.raw

247 <210> SEQ ID NO: 8
 248 <211> LENGTH: 27
 249 <212> TYPE: PRT
 250 <213> ORGANISM: Saccharomyces cerevisiae
 252 <400> SEQUENCE: 8
 253 Asp Ser Asn Gly Asn Ile Gln Gly Pro Phe Gly Thr Asn Asn Met Ser
 254 1 5 10 15
 255 Gln Trp Tyr Gln Gly Gly Tyr Phe Thr Pro Thr
 256 20 25
 259 <210> SEQ ID NO: 9
 260 <211> LENGTH: 17
 261 <212> TYPE: PRT
 262 <213> ORGANISM: Artificial Sequence
 264 <220> FEATURE:
 265 <223> OTHER INFORMATION: Motif in CD2 binding region of CD2BP2
 W--> 268 <221> NAME/KEY: VARIANT
 269 <222> LOCATION: 3, 4, 5, 6, 7, 8, 9, 10, 12, 13, 14
 270 <223> OTHER INFORMATION: Xaa = Any Amino Acid
 W--> 272 <400> 9
 W--> 273 Gly Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Trp Xaa Xaa Xaa Gly Thr
 274 1 5 10 15
 275 Phe
 279 <210> SEQ ID NO: 10
 280 <211> LENGTH: 6
 281 <212> TYPE: PRT
 282 <213> ORGANISM: Artificial Sequence
 284 <220> FEATURE:
 285 <223> OTHER INFORMATION: CD2BP2 binding region
 288 <400> SEQUENCE: 10
 289 Pro Pro Pro Gly His Arg
 290 1 5
 293 <210> SEQ ID NO: 11
 294 <211> LENGTH: 70
 295 <212> TYPE: PRT
 296 <213> ORGANISM: Homo sapiens
 298 <400> SEQUENCE: 11
 299 Pro Pro Pro Pro Pro Gly His Arg Ser Gln Ala Pro Ser His Arg Pro
 300 1 5 10 15
 301 Pro Pro Pro Gly His Arg Val Gln His Gln Pro Gln Lys Arg Pro Pro
 302 20 25 30
 303 Ala Pro Ser Gly Thr Gln Val His Gln Gln Lys Gly Pro Pro Leu Pro
 304 35 40 45
 305 Arg Pro Arg Val Gln Pro Lys Pro Pro His Gly Ala Ala Glu Asn Ser
 306 50 55 60
 307 Leu Ser Pro Ser Ser Asn
 308 65 70
 311 <210> SEQ ID NO: 12
 312 <211> LENGTH: 8
 313 <212> TYPE: DNA